Contents

No. 1 1–168 issued December II 1991
No. 2 169–336 issued January 1992
No. 3 337–498 issued February 1992

Adeline M-T → Ozier-Kalogeropoulos O 7
Apel K → Bunge S 460
Araki H, Awane K, Ogawa N, Oshima Y: The *CDC26* gene of *Saccharomyces cerevisiae* is required for cell growth only at high temperature 329
Asai T, Chen CP, Nagata T, Takanami M, Imai M: Transcription in vivo within the replication origin of the *Escherichia coli* chromosome: a mechanism for activating initiation of replication 169
Awane K → Araki H 329

Baker R → Chee MS 106
Belliard G → Maillot-Vernier P 33
Benveniste P → Maillot-Vernier P 33
Bitter GA, Chang KKH, Egan KM: A multi-component upstream activation sequence of the *Saccharomyces cerevisiae* glyceraldehyde-3-phosphate dehydrogenase gene promoter 22
Blowers AD → McElroy D 150
Bockrath R → Li BH 480
Boe L: Translational errors as the cause of mutations in *Escherichia coli* 469
Bowman SB, Zaman Z, Collinson LP, Brown AJP, Dawes IW: Positive regulation of the *LPD1* gene of *Saccharomyces cerevisiae* by the HAP2/HAP3/HAP4 activation system 296
Braun HP, Emmermann M, Kruft V, Schmitz UK: Cytochrome c_1 from potato: a protein with a presequence for targeting to the mitochondrial intermembrane space 217
Brendel M → Richter D 194
Brinkmann K → Friemann A 411
Brizzard BL, Schnepf HE, Kronstad JW: Expression of the *crylB* crystal protein gene of *Bacillus thuringiensis* 59
Brown AJP → Bowman SB 296
Bruijn FJ de → Pawlowski K 124
Buchel AS → Rommens CMT 433
Bunge S, Wolters J, Apel K: A comparison of leaf thionin sequences of barley cultivars and wild barley species 460

Cervera M → Vinós J 385
Chang KKH → Bitter GA 22
Chaubet N → Lepetit M 276
Chee MS, Rizos H, Henderson BR, Baker R, Stewart TS: Subfamilies of serine tRNA genes in the bovine genome 106
Chen CP → Asai T 169
Clutterbuck AJ, Stark MS, Gupta G: An intragenic map of the *brlA* locus of *Aspergillus nidulans* 212
Collin J → Ozier-Kalogeropoulos O 7
Collinson LP → Bowman SB 296

Dawes IW → Bowman SB 296
Daza A → Vigal T 88
Dean D → Kennedy C 494
De Mot R, Proost P, Van Damme J, Vanderleyden J: Homology of the root adhesin of *Pseudomonas fluorescens* OE 28.3 with porin F of *P. aeruginosa* and *P. syringae* 489
Doi RH → Hamamoto T 472
Drabble WT → Tesfa-Selas F 256
Dumas C → Lee RW 53
Duport C, Jouanneau Y, Vignais PM: Transcriptional analysis and promoter mapping of the *fdxA* gene which encodes the 7 Fe ferredoxin (FdII) of *Rhodobacter capsulatus* 323
Dürrenberger M → Spurio R 201
Dwyer KG, Lalonde BA, Nasrallah JB, Nasrallah ME: Structure and expression of *AtS1*, an *Arabidopsis thaliana* gene homologous to the *S*-locus related genes of *Brassica* 442

Egan KM → Bitter GA 22
Ehling M → Lepetit M 276
Elmerich Cl → Vieille Cl 375
Emmermann M → Braun HP 217

Falconi M → Spurio R 201
Fantes PA → Hughes DA 401
Farman ML, Oliver RP: Transformation frequencies are enhanced and vector DNA is targeted during retransformation of *Leptosphaeria maculans*, a fungal plant pathogen 243
Fasiolo F → Ozier-Kalogeropoulos O 7
Feix G → Quayle T 369
Ferretti JJ → Yu C-E 161
Flavell AJ, Smith DB, Kumar A: Extreme heterogeneity of *Ty1-copia* group retrotransposons in plants 233
Fluhr R → Segal G 179
Foong F → Hamamoto T 472
Foss HM, Selker EU: Efficient DNA pairing in a *Neurospora* mutant defective in chromosome pairing 49
Franco L → Matallana E 395
Freundlich M → Ramani N 248
Friemann A, Brinkmann K, Hachtel W: Sequence of a cDNA encoding nitrite reductase from the tree *Betula pendula* and identification of conserved protein regions 411

García-González MD → Vigal T 88
Garesse R → Vinós J 385
Geerse RH → Niersbach M 332
Gigot C → Lepetit M 276
Gil JA → Vigal T 88
Goebel W → Haas A 313
Gohl HP, Hausner W, Thomm M: Cell-free transcription of the *nifH1* gene of *Methanococcus thermolithotrophicus* indicates that promoters of archaeal *nif* genes share basic features with the methanogen consensus promoter 286
Goldschmidt-Clermont M → Monod C 449
Gondet L → Maillot-Vernier P 33
Gualerzi CO → Spurio R 201
Gupta G → Clutterbuck AJ 212

Haaren MJJ van → Rommens CMT 433
Haas A, Goebel W: Cloning of a superoxide dismutase gene from *Listeria ivanovil* by functional complementation in *Escherichia coli* and characterization of the gene product 313
Hachtel W → Friemann A 411
Halfter U, Morris P-C, Willmitzer L: Gene targeting in *Arabidopsis thaliana* 186
Hamamoto T, Foong F, Shoseyov O, Doi RH: Analysis of functional domains of endoglucanases from *Clostridium cellulovorans* by gene cloning, nucleotide sequencing and chimeric protein construction 472
Hanafusa T, Kinashi H: The structure of an integrated copy of the giant linear plasmid SCP1 in the chromosome of *Streptomyces coelicolor* 2612 363
Hausner W → Gohl HP 286
Hawker KL, Montague P, Kinghorn JR: Nitrate reductase and nitrite reductase transcript levels in various mutants of *Aspergillus nidulans*: confirmation of autogenous regulation 485
Hayes S: Mapping ethanol-induced deletions 139
Heidmann I → Meyer P 345
Henderson BR → Chee MS 106
Hille J → Rommens CMT 433
Hiom KJ, Sedgwick SG: Alleviation of *Eco*K DNA restriction in *Escherichia coli* and involvement of *umuDC* activity 265
Hirsch HJ → Niersbach M 332
Huang L → Ramani N 248
Hughes DA, MacNeill SA, Fantes PA: Molecular cloning and sequence analysis of $cdc27^+$ required for the G_2-M transition in the fission yeast *Schizosaccharomyces pombe* 401

Ikeda E → Yoshida S 337
Imai M → Asai T 169
Itoh Y, Matsumoto H: Mutations affecting regulation of the anabolic *argF* and the catabolic *aru* genes in *Pseudomonas aeruginosa* PAO 417

Jenes B → McElroy D 150
Jouanneau Y → Duport C 323
Jueterbock W-R → Quiñones A 81

Kahn ML → Udvardi MK 97
Kennedy C, Dean D: The *nifU*, *nif S* and *nifV* gene products are required for activ-

ity of all three nitrogenases of *Azotobacter vinelandii* 494
Kinashi H → Hanafusa T 363
King PJ → Souza L de 65
Kinghorn JR → Hawker KL 485
Kirchner J → Li BH 480
Klosse U → Pawlowski K 124
Kochert G → Zhao X 353
Krajewski WA, Luchnik AN: High rotational mobility of DNA in animal cells and its modulation by histone acetylation 17
Kreuzaler F → Niersbach M 332
Kronstad JW → Brizzard BL 59
Kruft V → Braun HP 217
Kumar A → Flavell AJ 233
Kwasniewski M → Li BH 480

Lacroute F → Ozier-Kalogeropoulos O 7
Lalonde BA → Dwyer KG 442
La Teana A → Spurio R 201
Lee RW, Dumas C, Lemieux C, Turmel M: Cloning and characterization of the *Chlamydomonas moewusii* mitochondrial genome 53
Lemieux C → Lee RW 53
Lepetit M, Ehling M, Chaubet N, Gigot C: A plant histone gene promoter can direct both replication-dependent and -independent gene expression in transgenic plants 276
Li BH, Kwasniewski M, Kirchner J, Bockrath R: RexAB proteins of bacteriophage λ enhance the effect of photolyase-dimer complexes on *lacZ* gene expression in *Escherichia coli* 480
Linn F → Meyer P 345
Liu C-N, Rubenstein I: Genomic organization of an α-zein gene cluster in maize 304
Luchnik AN → Krajewski WA 17

MacNeill SA → Hughes DA 401
Maillot-Vernier P, Gondet L, Schaller H, Benveniste P, Belliard G: Genetic study and further biochemical characterization of a tobacco mutant that overproduces sterols 33
Mansouri K → Pissowotzki K 113
Marco R → Vinós J 385
Maroto M → Vinós J 385
Martín JF → Vigal T 88
Matallana E, Franco L, Pérez-Ortín JE: Chromatin structure of the yeast *SUC2* promoter in regulatory mutants 395
Matsumoto H → Itoh Y 417
McElroy D, Blowers AD, Jenes B, Wu R: Construction of expression vectors based on the rice actin 1 (*Act1*) 5′ region for use in monocot transformation 150
Messer W → Quiñones A 81
Meyer H → Meyer P 345
Meyer P, Linn F, Heidmann I, Meyer HZA, Niedenhof I, Saedler H: Endogenous and environmental factors influence 35S promoter methylation of a maize A1 gene construct in transgenic petunia and its colour phenotype 345
Mitsui H, Takahashi H: Cohesive single-stranded ends of *Streptomyces* temperate bacteriophage R4 360
Mitsuzawa H → Yoshida S 337
Mol JNM → Rommens CMT 433
Monod C, Goldschmidt-Clermont M, Rochaix JD: Accumulation of chloroplast *psbB* RNA requires a nuclear factor in *Chlamydomonas reinhardtii* 449
Montague P → Hawker KL 485
Morris P-C → Halfter U 186

Nagata T → Asai T 169
Nasrallah JB → Dwyer KG 442
Nasrallah ME → Dwyer KG 442
Niedenhof I → Meyer P 345
Niegemann E → Richter D 194
Niersbach M, Kreuzaler F, Geerse RH, Postma PW, Hirsch HJ: Cloning and nucleotide sequence of the *Escherichia coli* K-12 *ppsA* gene, encoding PEP synthase 332
Nijkamp HJ → Rommens CMT 433

Ogawa N → Araki H 329
Oliver RP → Farman ML 243
Ori N → Segal G 179
Oshima Y → Araki H 329
Ozier-Kalogeropoulos O, Fasiolo F, Adeline M-T, Collin J, Lacroute F: Cloning, sequencing and characterization of the *Saccharomyces cerevisiae URA7* gene encoding CTP synthetase 7

Pawlowski K, Klosse U, Bruijn FJ de: Characterization of a novel *Azorhizobium caulinodans* ORS571 two-component regulatory system, NtrY/NtrX, involved in nitrogen fixation and metabolism 124
Pérez-Ortín JE → Matallana E 395
Piepersberg W → Pissowotzki K 113
Pissowotzki K, Mansouri K, Piepersberg W: Genetics of streptomycin production in *Streptomyces griseus:* molecular structure and putative function of genes *strELMB2N* 113
Pon CL → Spurio R 201
Postma PW → Niersbach M 332
Potrykus I → Takamizo T 1
Proost P → De Mot R 489

Quayle T, Feix G: Functional analysis of the − 300 region of maize zein genes 369
Quiñones A, Jueterbock W-R, Messer W: DNA lesions that block DNA replication are responsible for the *dnaA* induction caused by DNA damage 81

Raju NB → Schroeder AL 41
Ramani N, Huang L, Freundlich M: In vitro interactions of integration host factor with the *ompF* promoter-regulatory region of *Escherichia coli* 248
Richter D, Niegemann E, Brendel M: Molecular structure of the DNA cross-linke repair gene *SNM1* (*PSO2*) of the yeast *Saccharomyces cerevisiae* 194
Rieping M, Schöffl F: Synergistic effect of upstream sequences, CCAAT box elements, and HSE sequences for enhanced expression of chimaeric heat shock genes in transgenic tobacco 226
Rizos H → Chee MS 106
Rochaix JD → Monod C 449
Rommens CMT, Haaren MJJ van, Buchel AS, Mol JNM, Tunen AJ van, Nijkamp HJJ, Hille J: Transactivation of *Ds* by *Ac*-transposase gene fusions in tobacco 433
Rubenstein I → Liu C-N 304

Saedler H → Meyer P 345
Sarfatti M → Segal G 179
Schaffer MA → Segal G 179
Schaller H → Maillot-Vernier P 33
Schmitz UK → Braun HP 217
Schnepf HE → Brizzard BL 59
Schöffl F → Rieping M 226
Schroeder AL, Raju NB: *mei-2,* a mutagen-sensitive mutant of *Neurospora* defective in chromosome pairing and meiotic recombination 41
Sedgwick SG → Hiom KJ 265
Segal G, Sarfatti M, Schaffer MA, Ori N, Zamir D, Fluhr R: Correlation of genetic and physical structure in the region surrounding the I_2 *Fusarium oxysporum* resistance locus in tomato 179
Selker EU → Foss HM 49
Søgaard-Andersen L, Valentin-Hansen P: Restored DNA-binding of the cAMP-CRP activator complex reestablishes negative regulation by the CytR repressor in the *deoP2* promoter in *Escherichia coli* 76
Shoseyov O → Hamamoto T 472
Smith DB → Flavell AJ 233
Souza L de, King PJ: Mutants of *Nicotiana plumbaginifolia* with increased sensitivity to auxin 65
Spangenberg G → Takamizo T 1
Spurio R, Dürrenberger M, Falconi M, La Teana A, Pon CL, Gualerzi CO: Lethal overproduction of the *Escherichia coli* nucleoid protein H-NS: ultramicroscopic and molecular autopsy 201
Stark MS → Clutterbuck AJ 212
Stewart TS → Chee MS 106
Suginobu K → Takamizo T 1

Takahashi H → Mitsui H 360
Takamizo T, Spangenberg G, Suginobu K, Potrykus I: Intergeneric somatic hybridization in Gramineae: somatic hybrid plants between tall fescue (*Festuca arundinacea* Schreb.) and Italian ryegrass (*Lolium multiflorum* Lam.) 1
Takanami M → Asai T 169
Tanaka K → Uesono Y 426
Tesfa-Selas F, Drabble WT: Regulation of the *gua* operon of *Escherichia coli* by the DnaA protein 256
Thomm M → Gohl HP 286
Toh-e A → Uesono Y 426
Tokai M → Uesono Y 426
Tunen AJ van → Rommens CMT 433
Turmel M → Lee RW 53

Udvardi MK, Kahn ML: Isolation and analysis of a cDNA clone that encodes an alfalfa (*Medicago sativa*) aspartate aminotransferase 97
Uesono Y, Tokai M, Tanaka K, Toh-e A:

Negative regulators of the PHO system of *Saccharomyces cerevisiae*: characterization of *PHO80* and *PHO85* 426
Uno I → Yoshida S 337

Valentin-Hansen P → Søgaard-Andersen L 76
Van Damme J → De Mot R 489
Vanderleyden J → De Mot R 489
Vieille Cl, Elmerich C: Characterization of an *Azospirillum brasilense* Sp7 gene homologous to *Alcaligenes eutrophus phbB* and to *Rhizobium meliloti nodG* 375
Vigal T, Gil JA, Daza A, García-González MD, Villadas P, Martín JF: Effects of replacement of promoters and modification of the leader peptide region of the *amy* gene of *Streptomyces griseus* on synthesis and secretion of α-amylase by *Streptomyces lividans* 88
Vignais PM → Duport C 323
Villadas P → Vigal T 88
Vinós J, Maroto M, Garesse R, Marco R, Cervera M: *Drosophila melanogaster* paramyosin: developmental pattern, mapping and properties deduced from its complete coding sequence 385

Willmitzer L → Halfter U 186
Wolters J → Bunge S 460
Wu R → McElroy D 150

Yoshida S, Ikeda E, Uno I, Mitsuzawa H: Characterization of a staurosporine- and temperature-sensitive mutant, *stt1*, of *Saccharomyces cerevisiae*: *STT1* is allelic to *PKC1* 337
Yu C-E, Ferretti JJ: Molecular characterization of new group A streptococcal bacteriophages containing the gene for streptococcal erythrogenic toxin A (*speA*) 161

Zaman Z → Bowman SB 296
Zamir D → Segal G 179
Zhao X, Kochert G: Characterization and genetic mapping of a short, highly repeated, interspersed DNA sequence from rice (*Oryza sativa* L.) 353

Indexed in *Current Contents*